IN THE CLAIMS

Amend the claims as follows.

Claims 1-12 (canceled)

13. (Currently Amended) A method for the detection of acute respiratory tract infection in a sample comprising the simultaneous amplification of several target nucleotide sequences which may be present in said sample, said method comprising contacting said sample with a mixture of nucleic acid primers under conditions whereby said primers bind to corresponding target nucleotide sequences when present in said sample and allow said simultaneous amplification, said mixture of nucleic acid primers comprising at least one primer set from each one of the following gene regions:

D1 cont'd

the F1 subunit of the fusion glycoprotein gene of RSV,

the hemagglutininneuraminidase gene of PIV-1,

the 5' noncoding region of the PIV-3 fusion protein gene,

the non-structural protein gene of influenza A, and

the non-structural protein gene of influenza B,

and said mixture further comprising at least one primer set from at least one of the following further genes:

16S rRNA sequence of *M. pneumoniae*,

spacer sequence of *M. pneumoniae*,

16S rRNA sequence of *C. pneumoniae*,

spacer sequence of *C. pneumoniae*,

the 5' noncoding region of enterovirus, and

the hexon gene of adenoviruses.

14. (Previously Presented) A method according to claim 13 wherein the gene region of said 16S rRNA sequence of *M. pneumoniae* and said 16S rRNA sequence of *C. pneumoniae* are the 16S-23S spacer region of *M. pneumoniae* and the 16S-23S spacer region of *C. pneumoniae*, respectively.

15. (Previously Presented) A method according to claim 13 wherein said mixture further comprises at least one primer set from the 16S-23S spacer region of *B. pertussis* and *B. parapertussis*.

16. (Previously Presented) A method according to claim 14 wherein said primer mixture further comprises at least one primer set from the 16S-23S spacer region of *B. pertussis* and *B. parapertussis*

17. (Currently Amended) A method according to claim 13 wherein at least one of said at least one primer set is selected from the group consisting of:

for the 5' noncoding region of enterovirus, SEQ ID NOs: 35 and 36;

for ~~16S rRNA~~ spacer sequence of *M. pneumoniae*, SEQ ID NOs:17 and 19, or SEQ ID NOs: 18 and 19~~, or SEQ ID NOs: 37 and 38~~;

for 16S r RNA sequence of *M. pneumoniae*, SEQ ID NOs: 37 and 38;

for the non-structural protein gene of influenza A, SEQ ID NOs: 39 and 40;

for the non-structural protein gene of influenza B, SEQ ID NOs: 41 and 42;

for the hexon gene of adenoviruses, SEQ ID NOs: 43 and 44;

for 16S rRNA sequence of *C. pneumoniae*, ~~SEQ ID NOs: 20 and 21 or~~ SEQ ID NOs: 45 and 46;

for spacer sequence of *C. pneumoniae*, SEQ ID NOs: 20 and 21;

for the hemagglutininneuraminidase gene of PIV-1, SEQ ID NOs: 47 and 48;

for the 5' noncoding region of the PIV-3 fusion protein gene, SEQ ID NOs: 49 and 50; and

for the F1 subunit of the fusion glycoprotein gene of RSV, SEQ ID NOs: 51 and 52.

18. (Previously Presented) A method according to claim 13 wherein said method comprises a process of reverse transcription prior to said contacting, followed by a process of amplification.

19. (Previously Presented) A method according to claim 14 wherein said method comprises a process of reverse transcription prior to said contacting, followed by a process of amplification.

20. (Previously Presented) A method according to claim 15 wherein said method comprises a process of reverse transcription prior to said contacting, followed by a process of amplification.

21. (Previously Presented) A method according to claim 13 wherein products of said amplification are subsequently detected using a probe.

22. (Previously Presented) A method according to claim 14 wherein products of said amplification are subsequently detected using a probe.

23. (Previously Presented) A method according to claim 15 wherein products of said amplification are subsequently detected using a probe.

24. (Previously Presented) A method according to claim 20 wherein products of said amplification are subsequently detected using a probe.

25. (Previously Presented) A method according to claim 21 wherein at least one of said probes is selected from the group consisting of a sequence of SEQ ID NOs:1, 4-34, or 53- 56, a sequence complementary to a sequence of SEQ ID NOs:1, 4-34, or 53-56, a RNA sequence form of a sequence of SEQ ID NOs:1, 4-34, or 53- 56 wherein T is replaced by U, and a RNA sequence form of a sequence complementary to a sequence of SEQ ID NOs:1, 4-34, or 53- 56 wherein T is replaced by U.

26. (Previously Presented) A method according to claim 22 wherein at least one of said probes is selected from the group consisting of a sequence of SEQ ID NOs:1, 4-34, or 53- 56, a sequence complementary to a sequence of SEQ ID NOs:1, 4-34, or 53- 56, a RNA sequence form of a sequence of SEQ ID NOs:1, 4-34, or 53- 56 wherein T is replaced by U, and a RNA sequence form of a sequence complementary to a sequence of SEQ ID NOs:1, 4-34, or 53- 56 wherein T is replaced by U.

27. (Previously Presented) A method according to claim 23 wherein at least one of said probes is selected from the group consisting of a sequence of SEQ ID NOs:1, 4-34, or 53- 56, a sequence complementary to a sequence of SEQ ID NOs:1, 4-34, or 53- 56, a RNA sequence form of a sequence of SEQ ID NOs:1, 4-34, or 53- 56 wherein T is replaced by U, and a RNA sequence form of a sequence complementary to a sequence of SEQ ID NOs:1, 4-34, or 53- 56 wherein T is replaced by U.

28. (Previously Presented) A method according to claim 24 wherein at least one of said probes is selected from the group consisting of a sequence of SEQ ID NOs:1, 4-34, or 53- 56, a sequence complementary to a sequence of SEQ ID NOs:1, 4-34, or 53- 56,

a RNA sequence form of a sequence of SEQ ID NOs:1, 4-34, or 53- 56 wherein T is replaced by U, and a RNA sequence form of a sequence complementary to a sequence of SEQ ID NOs:1, 4-34, or 53- 56 wherein T is replaced by U.

29. (Previously Presented) A method according to claim 21 wherein products of said amplification are immobilised on a solid support.

30. (Previously Presented) A method according to claim 22 wherein products of said amplification are immobilised on a solid support.

31. (Previously Presented) A method according to claim 13 wherein products of said amplification are sequenced.

32. (Previously Presented) A method according to claim 14 wherein products of said amplification are sequenced.

33. (Previously Presented) A method according to claim 15 wherein products of said amplification are sequenced.

34. (Previously Presented) A method according to claim 16 wherein products of said amplification are sequenced.

35. (Previously Presented) A method according to claim 17 wherein products of said amplification are sequenced.

36. (Currently Amended) A method according to claim 15 wherein at least one of said at least one primer set is selected from the group consisting of:

for the 5' noncoding region of enterovirus, SEQ ID NOs: 35 and 36;

for ~~16S rRNA~~ spacer sequence of *M. pneumoniae*, SEQ ID NOs:17 and 19, or SEQ ID NOs: 18 and 19~~, or SEQ ID NOs: 37 and 38~~;

for 16S r RNA sequence of *M. pneumoniae*, SEQ ID NOs: 37 and 38;

for the non-structural protein gene of influenza A, SEQ ID NOs: 39 and 40;

for the non-structural protein gene of influenza B, SEQ ID NOs: 41 and 42;

for the hexon gene of adenoviruses, SEQ ID NOs: 43 and 44;

for 16S rRNA sequence of *C. pneumoniae*, ~~SEQ ID NOs: 20 and 21 or~~ SEQ ID NOs: 45 and 46;

for spacer sequence of *C. pneumoniae*, SEQ ID NOs: 20 and 21;

for the hemagglutininneuraminidase gene of PIV-1, SEQ ID NOs: 47 and 48;

for the 5' noncoding region of the PIV-3 fusion protein gene, SEQ ID NOs: 49 and 50;

for the F1 subunit of the fusion glycoprotein gene of RSV, SEQ ID NOs: 51 and 52, and

for the 16S-23S spacer region of *B. pertussis* and *B. parapertussis*, SEQ ID NOs: 22 and 23.

37. (Previously Presented) A nucleic acid primer selected from the group consisting of SEQ ID NOs: 35, 36, 17, 18, 19, 37, 38, 39, 40, 41, 42, 43, 44, 20, 21, 45, 46, 47, 48, 49, 50, 51, 52, 22, or 23; a sequence complementary to a sequence of SEQ ID NOs: 35, 36, 17, 18, 19, 37, 38, 39, 40, 41, 42, 43, 44, 20, 21, 45, 46, 47, 48, 49, 50, 51, 52, 22, or 23; a RNA sequence form of a sequence of SEQ ID NOs: 35, 36, 17, 18, 19, 37, 38, 39, 40, 41, 42, 43, 44, 20, 21, 45, 46, 47, 48, 49, 50, 51, 52, 22, or 23 wherein T is replaced by U, and a RNA sequence form of a sequence complementary to a sequence of SEQ ID NOs: 35, 36, 17, 18, 19, 37, 38, 39, 40, 41, 42, 43, 44, 20, 21, 45, 46, 47, 48, 49, 50, 51, 52, 22, or 23 wherein T is replaced by U.

38. (Previously Presented) A nucleic acid primer set selected from the group of primer sets consisting of:

SEQ ID NOs: 35 and 36, SEQ ID NOs:17 and 19, SEQ ID NOs:18 and19, SEQ ID NOs:37 and 38, SEQ ID NOs:39 and 40, SEQ ID NOs: 41and 42, SEQ ID NOs: 43 and 44, SEQ ID NOs: 20 and 21, SEQ ID NOs:45 and 46, SEQ ID NOs:47 and 48, SEQ ID NOs:49 and 50, SEQ ID NOs:51and 52, SEQ ID NOs:22 and 23,

SEQ ID NOs: 35 and 36, SEQ ID NOs:17 and 19, SEQ ID NOs:18 and19, SEQ ID NOs:37 and 38, SEQ ID NOs:39 and 40, SEQ ID NOs: 41and 42, SEQ ID NOs: 43 and 44, SEQ ID NOs: 20 and 21, SEQ ID NOs:45 and 46, SEQ ID NOs:47 and 48, SEQ ID NOs:49 and 50, SEQ ID NOs:51and 52, SEQ ID NOs:22 and 23, wherein at least one of said sequences is a sequence complementary to said SEQ ID NO:,

SEQ ID NOs: 35 and 36, SEQ ID NOs:17 and 19, SEQ ID NOs:18 and19, SEQ ID NOs:37 and 38, SEQ ID NOs:39 and 40, SEQ ID NOs: 41and 42, SEQ ID NOs: 43 and 44, SEQ ID NOs: 20 and 21, SEQ ID NOs:45 and 46, SEQ ID NOs:47 and 48, SEQ ID NOs:49 and 50, SEQ ID NOs:51and 52, SEQ ID NOs:22 and 23, wherein at least one of said sequences is a RNA sequence form of said SEQ ID NO: wherein T of said sequence is replaced with U, and

SEQ ID NOs: 35 and 36, SEQ ID NOs:17 and 19, SEQ ID NOs:18 and19, SEQ ID NOs:37 and 38, SEQ ID NOs:39 and 40, SEQ ID NOs: 41and 42, SEQ ID NOs: 43 and 44, SEQ ID NOs: 20 and 21, SEQ ID NOs:45 and 46, SEQ ID NOs:47 and 48, SEQ ID NOs:49 and 50, SEQ ID NOs:51and 52, SEQ ID NOs:22 and 23, wherein at least one of said sequences is complementary to said SEQ ID NO: and is a RNA sequence form of said sequence wherein T of said complementary sequence is replaced with U.

39. (Previously Presented) A collection of nucleic acid primer sets comprising at least two primer sets of claim 38 said primer sets being capable of binding to distinct gene regions.

40. (Previously Presented) A collection of nucleic acid primer sets comprising at least five primer sets of claim 38 said primer sets being capable of binding to distinct gene regions.

41. (Previously Presented) A collection of nucleic acid primer sets comprising at least nine primer sets of claim 38, said primer sets being capable of binding to distinct gene regions.

42. (Previously Presented) A nucleic acid probe selected from the group consisting of SEQ ID NOs: 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33 and 34.

43. (Previously Presented) A collection of a nucleic acid a primer set of claim 38 and a nucleic acid probe selected from the group consisting of SEQ ID NOs: 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33 and 34.

44. (Previously Presented) A kit comprising the collection of claim 39.

45. (Previously Presented) A kit comprising the primer set of claim 38.

46. (Previously Presented) A kit comprising a collection of claim 43.

47. (Previously Presented) A nucleic acid probe selected from the group consisting SEQ ID NOs:1, 4-34, or 53- 56, a sequence complementary to a sequence of SEQ ID NOs:1, 4-34, or 53- 56, a RNA sequence form of a sequence of SEQ ID NOs:1, 4-34, or 53- 56 wherein T is replaced by U, and a RNA sequence form of a sequence

complementary to a sequence of SEQ ID NOs:1, 4-34, or 53-56 wherein T is replaced by U.

48. (Previously Presented) A collection of a nucleic acid a primer set of claim 38 and a nucleic acid probe selected from the group consisting of SEQ ID NOs:1, 4-34, or 53- 56, a sequence complementary to a sequence of SEQ ID NOs:1, 4-34, or 53- 56, a RNA sequence form of a sequence of SEQ ID NOs:1, 4-34, or 53- 56 wherein T is replaced by U, and a RNA sequence form of a sequence complementary to a sequence of SEQ ID NOs:1, 4-34, or 53-56 wherein T is replaced by U.

49. (Previously Presented) A kit comprising the collection of claim 48.